

09/868131

SEQUENCE LISTING

B1
<110> Cohen, Philip
Kobayashi, Takayasu
Deak, Maria

<120> Methods

<130> 002.00160

<140> US 09/868,131

<141> 2001-06-14

<150> PCT/GB99/04232

<151> 1999-12-14

sub C17
<150> GB 9919676.8

<151> 1999-08-19

<150> US 60/112,217

<151> 1998-12-14

<160> 44

<170> PatentIn Ver. 2.0

<210> 1

<211> 367

<212> PRT

<213> h. sapiens

<400> 1

Met Asn Ser Ser Pro Ala Gly Thr Pro Ser Pro Gln Pro Ser Arg Ala
1 5 10 15

Asn Gly Asn Ile Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Gln Pro
20 25 30

Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
35 40 45

Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
50 55 60

Val Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile
65 70 75 80

Met	Ala	Glu	Arg	Ser	Val	Leu	Leu	Lys	Asn	Val	Arg	His	Pro	Phe	Leu	
				85					90					95		
Val	Gly	Leu	Arg	Tyr	Ser	Phe	Gln	Thr	Pro	Glu	Lys	Leu	Tyr	Phe	Val	
			100					105					110			
Leu	Asp	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Gln	Arg	Glu	
		115					120					125				
Arg	Arg	Phe	Leu	Glu	Pro	Arg	Ala	Arg	Phe	Tyr	Ala	Ala	Glu	Val	Ala	
		130					135				140					
Ser	Ala	Ile	Gly	Tyr	Leu	His	Ser	Leu	Asn	Ile	Ile	Tyr	Arg	Asp	Leu	
145					150					155					160	
Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Cys	Gln	Gly	His	Val	Val	Leu	Thr	
			165						170					175		
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Val	Glu	Pro	Glu	Asp	Thr	Thr	Ser	
			180					185					190			
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Arg	Lys	
		195					200					205				
Glu	Pro	Tyr	Asp	Arg	Ala	Val	Asp	Trp	Trp	Cys	Leu	Gly	Ala	Val	Leu	
		210				215					220					
Tyr	Glu	Met	Leu	His	Gly	Leu	Pro	Pro	Phe	Tyr	Ser	Gln	Asp	Val	Ser	
225					230					235					240	
Gln	Met	Tyr	Glu	Asn	Ile	Leu	His	Gln	Pro	Leu	Gln	Ile	Pro	Gly	Gly	
				245					250					255		
Arg	Thr	Val	Ala	Ala	Cys	Asp	Leu	Leu	Gln	Ser	Leu	Leu	His	Lys	Asp	
			260					265					270			
Gln	Arg	Gln	Arg	Leu	Gly	Ser	Lys	Ala	Asp	Phe	Leu	Glu	Ile	Lys	Asn	
		275					280					285				
His	Val	Phe	Phe	Ser	Pro	Ile	Asn	Trp	Asp	Asp	Leu	Tyr	His	Lys	Arg	
		290				295					300					
Leu	Thr	Pro	Pro	Phe	Asn	Pro	Asn	Val	Thr	Gly	Pro	Ala	Asp	Leu	Lys	
305					310					315					320	
His	Phe	Asp	Pro	Glu	Phe	Thr	Gln	Glu	Ala	Val	Ser	Lys	Ser	Ile	Gly	
				325					330					335		
Cys	Thr	Pro	Asp	Thr	Val	Ala	Ser	Ser	Ser	Gly	Ala	Ser	Ser	Ala	Phe	
			340					345					350			
Leu	Gly	Phe	Ser	Tyr	Ala	Pro	Glu	Asp	Asp	Asp	Ile	Leu	Asp	Cys		
		355					360					365				

<210> 2

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide

<400> 2

Asn	Glu	Glu	His	Asn	Ser	Thr	Thr	Ser	Thr	Phe	Cys	Gly	Thr	Pro	Glu
1				5					10					15	

<210> 3

<211> 367

<212> PRT

<213> Mus musculus

<400> 3

Met	Ala	Ser	Ser	Pro	Val	Gly	Val	Pro	Ser	Pro	Gln	Pro	Ser	Arg	Ala
1				5					10					15	

Asn	Gly	Asn	Ile	Asn	Leu	Gly	Pro	Ser	Ala	Asn	Pro	Asn	Ala	Arg	Pro
			20					25					30		

Thr	Asp	Phe	Asp	Phe	Leu	Lys	Val	Ile	Gly	Lys	Gly	Asn	Tyr	Gly	Lys
		35					40					45			

Val	Leu	Leu	Ala	Lys	Arg	Lys	Ser	Asp	Gly	Ala	Phe	Tyr	Ala	Val	Lys
	50					55					60				

Val	Leu	Gln	Lys	Lys	Ser	Ile	Leu	Lys	Asn	Lys	Glu	Gln	Asn	His	Ile
65					70					75					80

Met	Ala	Glu	Arg	Asn	Val	Leu	Leu	Lys	Asn	Val	Arg	His	Pro	Phe	Leu
				85					90					95	

Val	Gly	Leu	Arg	Tyr	Ser	Phe	Gln	Thr	Pro	Glu	Lys	Leu	Tyr	Phe	Val
			100					105					110		

Leu	Asp	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Gln	Arg	Glu	
	115						120					125				
Arg	Arg	Phe	Leu	Glu	Pro	Arg	Ala	Arg	Phe	Tyr	Thr	Ala	Glu	Val	Ala	
	130					135					140					
Ser	Ala	Ile	Gly	Tyr	Leu	His	Ser	Leu	Asn	Ile	Ile	Tyr	Arg	Asp	Leu	
	145				150				155						160	
Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Cys	Gln	Gly	His	Val	Val	Leu	Thr	
			165						170					175		
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Cys	Val	Glu	Pro	Glu	Glu	Thr	Thr	Ser	
			180					185					190			
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Arg	Lys	
		195					200					205				
Glu	Pro	Tyr	Asp	Arg	Ala	Val	Asp	Trp	Trp	Cys	Leu	Gly	Ala	Val	Leu	
	210					215					220					
Tyr	Glu	Met	Leu	His	Gly	Leu	Pro	Pro	Phe	Phe	Asn	Thr	Asp	Val	Ala	
	225				230					235					240	
Gln	Met	Tyr	Glu	Asn	Ile	Leu	His	Gln	Pro	Leu	Gln	Ile	Pro	Gly	Gly	
				245					250					255		
Arg	Thr	Val	Ala	Ala	Cys	Asp	Leu	Leu	Gln	Gly	Leu	Leu	His	Lys	Asp	
			260					265					270			
Gln	Arg	Gln	Arg	Leu	Gly	Ser	Lys	Glu	Asp	Phe	Leu	Asp	Ile	Lys	Asn	
		275					280					285				
His	Met	Phe	Phe	Ser	Pro	Ile	Asn	Trp	Asp	Asp	Leu	Tyr	His	Lys	Arg	
	290					295					300					
Leu	Thr	Pro	Pro	Phe	Asn	Pro	Asn	Val	Glu	Gly	Pro	Ala	Asp	Leu	Lys	
	305				310					315					320	
His	Phe	Asp	Pro	Glu	Phe	Thr	Gln	Glu	Ala	Val	Ser	Lys	Ser	Ile	Gly	
				325					330					335		
Cys	Thr	Pro	Asp	Thr	Val	Ala	Ser	Ser	Ser	Gly	Ala	Ser	Ser	Ala	Phe	
			340					345					350			
Leu	Gly	Phe	Ser	Tyr	Ala	Gln	Asp	Asp	Asp	Asp	Ile	Leu	Asp	Ser		
	355						360					365				

<210> 4

<211> 429

<212> PRT

<213> h. sapiens

<400> 4

Met	Ala	Leu	Lys	Ile	Pro	Ala	Lys	Arg	Ile	Phe	Gly	Asp	Asn	Phe	Asp
1				5					10					15	
Pro	Asp	Phe	Ile	Lys	Gln	Arg	Arg	Ala	Gly	Leu	Asn	Glu	Phe	Ile	Gln
			20					25					30		
Asn	Leu	Val	Arg	Tyr	Pro	Glu	Leu	Tyr	Asn	His	Pro	Asp	Val	Arg	Ala
		35					40					45			
Phe	Leu	Gln	Met	Asp	Ser	Pro	Lys	His	Gln	Ser	Asp	Pro	Ser	Glu	Asp
	50					55					60				
Glu	Asp	Glu	Arg	Ser	Ser	Gln	Lys	Leu	His	Ser	Thr	Ser	Gln	Asn	Ile
65					70					75					80
Asn	Leu	Gly	Pro	Ser	Gly	Asn	Pro	His	Ala	Lys	Pro	Thr	Asp	Phe	Asp
				85					90					95	
Phe	Leu	Lys	Val	Ile	Gly	Lys	Gly	Ser	Phe	Gly	Lys	Val	Leu	Leu	Ala
			100					105					110		
Lys	Arg	Lys	Leu	Asp	Gly	Lys	Phe	Tyr	Ala	Val	Lys	Val	Leu	Gln	Lys
		115					120					125			
Lys	Ile	Val	Leu	Asn	Arg	Lys	Glu	Gln	Lys	His	Ile	Met	Ala	Glu	Arg
	130					135					140				
Asn	Val	Leu	Leu	Lys	Asn	Val	Lys	His	Pro	Phe	Leu	Val	Gly	Leu	His
145					150					155					160
Tyr	Ser	Phe	Gln	Thr	Thr	Glu	Lys	Leu	Tyr	Phe	Val	Leu	Asp	Phe	Val
				165					170					175	
Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Gln	Arg	Glu	Arg	Ser	Phe	Pro
			180					185					190		
Glu	His	Arg	Ala	Arg	Phe	Tyr	Ala	Ala	Glu	Ile	Ala	Ser	Ala	Leu	Gly
		195					200					205			
Tyr	Leu	His	Ser	Ile	Lys	Ile	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn
	210					215					220				
Ile	Leu	Leu	Asp	Ser	Val	Gly	His	Val	Val	Leu	Thr	Asp	Phe	Gly	Leu
225					230					235					240
Cys	Lys	Glu	Gly	Ile	Ala	Ile	Ser	Asp	Thr	Thr	Thr	Thr	Phe	Cys	Gly
				245					250					255	

Thr Pro Glu Tyr Leu Ala Pro Glu Val Ile Arg Lys Gln Pro Tyr Asp
 260 265 270
 Asn Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
 275 280 285
 Tyr Gly Leu Pro Pro Phe Tyr Cys Arg Asp Val Ala Glu Met Tyr Asp
 290 295 300
 Asn Ile Leu His Lys Pro Leu Ser Leu Arg Pro Gly Val Ser Leu Thr
 305 310 315 320
 Ala Trp Ser Ile Leu Glu Glu Leu Leu Glu Lys Asp Arg Gln Asn Arg
 325 330 335
 Leu Gly Ala Lys Glu Asp Phe Leu Glu Ile Gln Asn His Pro Phe Phe
 340 345 350
 Glu Ser Leu Ser Trp Ala Asp Leu Val Gln Lys Lys Ile Pro Pro Pro
 355 360 365
 Phe Asn Pro Asn Val Ala Gly Pro Asp Asp Ile Arg Asn Phe Asp Thr
 370 375 380
 Ala Phe Thr Glu Glu Thr Val Pro Tyr Ser Val Cys Val Ser Ser Asp
 385 390 395 400
 Tyr Ser Ile Val Asn Ala Ser Val Leu Glu Ala Asp Asp Ala Phe Val
 405 410 415
 Gly Phe Ser Tyr Ala Pro Pro Ser Glu Asp Leu Phe Leu
 420 425

<210> 5

<211> 2146

<212> DNA

<213> h. sapiens

<400> 5

atgggttcag actttatgcc ctgaaaagat ccttcacagc ctggccatct tggacttctg 60
 gagctaccct ggctcacagg ggtcttggtg ccctgggtgt cccagttct tgaaaagaat 120
 cagcctggga ggggccacac cctgaccatc cccctttatc ccttctgaga tgtttgttag 180
 gaagtctggg tccaggggat atcatttctt gttccatcca tgcaggggtt gcttacctcg 240

ggtaggaaac cctcaggcgg tggcaggtgc acaggtaggg gaggatggag agggcagtgg 300
 tgccctgaagc cctggatggg eggagctgac cccccaacac caactctatc atgcctgctc 360
 ctccctgtcc ccccagagct gcctgatcat tgctacagaa tgaactctag cccagctggg 420
 accccaagtc cacagccctc cagggccaat gggaacatca acctggggcc ttcagccaac 480
 ccaaagtcac agcccacgga cttcgacttc ctcaaagtca tcggcaaagg gaactacggg 540
 aaggtcctac tggccaagcg caagtctgat ggggcgttct atgcagtga ggtactacag 600
 aaaaagtcca tcttaaagaa gaaagagcag agccacatca tggcagagcg cagtgtgctt 660
 ctgaagaacg tgcggcacc cttcctcgtg ggccctgcgt actccttcca gacacctgag 720
 aagctctact tcgtgctcga ctatgtcaac gggggagagc tcttcttcca cctgcagcgg 780
 gagcgccggt tcctggagcc ccgggccagg ttctacgctg ctgaggtggc cagcgccatt 840
 ggctacctgc actccctcaa catcatttac agggatctga aaccagagaa cattctcttg 900
 gactgccagg gacacgtggg gctgacggat tttggcctct gcaaggaagg ttagagacct 960
 gaagacacca catccacatt ctgtggtacc cctgagtact tggcacctga agtgcttcgg 1020
 aaagagcctt atgatcgagc agtggactgg tggcgcttgg gggcagtcct ctacgagatg 1080
 ctccatggcc tgccgccctt ctacagccaa gatgtatccc agatgtatga gaacattctg 1140
 caccagccgc tacagatccc eggaggccgg acagtggccg cctgtgacct cctgcaaagc 1200
 cttctccaca aggaccagag gcagcggctg ggctccaaag cagactttct tgagattaag 1260
 aaccatgtat tcttcagccc cataaactgg gatgacctgt accacaagag gctaactcca 1320
 cccttcaacc caaatgtgac aggacctgct gacttgaagc attttgacct agagttcacc 1380
 caggaagctg tgtccaagtc cattggctgt acccctgaca ctgtggccag cagctctggg 1440
 gcctcaagtg cattcctggg attttcttat gcgccagagg atgatgacat cttggattgc 1500
 tagaagagaa ggacctgtga aactactgag gccagctggg attagtaagg aattaccttc 1560
 agctgctagg aagagcgact caaactaaca atggcttcaa cgagaagcag gtttattttt 1620
 tccagcacat aaaagaaaaa taatgtttcg gagtccagga ctggcaggac aggtcatcag 1680
 atactcagag gctgtatctc tgccctgcca accttgacaa atggcttcca atggttaggtt 1740
 tgctacaaga tggttactgg agctctagct gcctattttg tgtttaggga agggaaaatg 1800
 gaggaaaggg gagaagagca aagggcgctt ttaaagagct ttcccaaaag ctccccccaa 1860

tgacttttgc ttccatctca ctaaccaccc acccctacct ggaatggagg ctgggaaatg 1920
 tggcttattt gctgggtacg tgactatccc taataacaaa ggggttttga ccctaagaca 1980
 ttaggggaga atgttgggta ggcagccagc cctcttttac catagggcct cctgggtgttt 2040
 ggattttgat ctcaatgtgt aaaatgacag agatgtaaca agctcatagg gtatcaatat 2100
 ctcttattgt tctatgttga aaaaaaaaaa aaaaaaaaaa aaaaaa 2146

<210> 6

<211> 2404

<212> DNA

<213> h. sapiens

<400> 6

ggtgtgctct tgagggatta aatgcaaaga gatcacacca tggactacaa ggaaagctgc 60
 ccaagtgtaa gcattcccag ctccgatgaa cacagagaga aaaagaagag gtttactgtt 120
 tataaagttc tggtttcagt ggggaagaagt gaatggtttg tcttcaggag atatgcagag 180
 tttgataaac tttataacac tttaaaaaaaa cagtttcctg ctatggccct gaagattcct 240
 gccaaagagaa tatttgggtga taattttgat ccagatttta ttaaacaag acgagcagga 300
 ctaaacgaat tcattcagaa cctagttagg tatccagaac tttataacca tccagatgtc 360
 agagcattcc ttcaaagga cagtccaaa caccagtcag atccatctga agatgaggat 420
 gaaagaagtt ctcagaagct aactctacc tcacagaaca tcaacctggg accgtctgga 480
 aatcctcatg ccaaaccaac tgactttgat ttcttaaaag ttattggaaa aggcagcttt 540
 ggcaaggttc ttcttgcaaa acggaaactg gatggaaaat tttatgctgt caaagtgtta 600
 cagaaaaaaaa tagttctcaa cagaaaagag caaaaacata ttatggctga acgtaatgtg 660
 ctcttgaaaa atgtgaaaca tccgtttttg gttggattgc attattcctt ccaaacaact 720
 gaaaagcttt attttgttct ggattttgtt aatggagggg agcttttttt ccacttacia 780
 agagaacggt cctttcctga gcacagagct aggttttacg ctgctgaaat tgctagtgca 840
 ttgggttact tacattccat caaaatagta tacagagact tgaaaccaga aaatattcct 900
 ttggattcag taggacatgt tgtcttaaca gattttgggc tttgtaaaga aggaattgct 960

atttctgaca ccactaccac attttgtggg acaccagagt atcttgcacc tgaagtaatt 1020
 agaaaacagc cctatgacaa tactgtagat tgggtggtgcc ttggggctgt tctgtatgaa 1080
 atgctgtatg gattgcctcc tttttattgc cgagatgttg ctgaaatgta tgacaatatc 1140
 cttcacaaac ccctaagttt gaggccagga gtgagtctta cagcctggtc cattctggaa 1200
 gaactcctag aaaaagacag gcaaaatcga cttggtgcca aggaagactt tcttgaaatt 1260
 cagaatcatc ctttttttga atcactcagc tgggctgacc ttgtacaaaa gaagattcca 1320
 ccaccattta atcctaattg ggctggacca gatgatatca gaaactttga cacagcattt 1380
 acagaagaaa cagttccata ttctgtgtgt gtatcttctg actattctat agtgaatgcc 1440
 agtgtattgg aggcagatga tgcattcgtt ggtttctctt atgcacctcc ttcagaagac 1500
 ttatttttgt gagcagtttg ccattcagaa accattgagc aaaataagtc tatagatggg 1560
 actgaaactt ctatttgtgt gaatatattc aaatatgtat aactagtgcc tcatttttat 1620
 atgtaatgat gaaaactatg aaaaaatgta ttttcttcta tgtgcaagaa aaatagggca 1680
 tttcaaagag ctgttttgat taaaatttat attcttgttt aataagctta tttttaaaca 1740
 atttaaaagc tattattctt agcattaacc tatttttaaa gaaacctttt ttgctattga 1800
 ctgttttttc cctctaagtt tacactaaca tctaccaag atagactgtt ttttaacagt 1860
 caatttcagt tcagctaaca tatattaata cttttgtaac tctttgctat ggcttttggt 1920
 atcacaccaa aactatgcaa ttggtacatg gttgtttaag aagaaaccgt atttttccat 1980
 gataaatcac tgtttgaaat atttggttca tgggtatgatc gaaatgtaaa agcataatta 2040
 acacattggc tgctagttaa caattggaat aactttattc tgcagatcat ttaagaagta 2100
 acaggccggg cgcggtggct cagcctgta atcccagcac tttgggaggc tgaggcgggc 2160
 agatcacctg aggtcaggag ttggagacca gctgaccaa catggacaaa cccgctctct 2220
 actaaaaata caaaattggc aggggtgtgtt ggcacatgcc tataatcca gctacttggg 2280
 aggctaaggc aggagaatcg cttgaacctg ggaggcggag gttgcagtga gccgagatcg 2340
 caccattgca ctctgcctg ggcaacaaga gtgaaactcc atctccaaaa aaaaaaaaaa 2400
 aaaa 2404

<210> 7

<211> 1834

<212> DNA

<213> h. sapiens

<400> 7

gaagagggca gagccgtgca tggggctgct ccccaggacc tgagcaggaa cctggagttt 60
tcagagctgc ctgatcattg ctacagaatg aactctagcc cagctgggac cccaagtcca 120
cagccctcca gggccaatgg gaacatcaac ctggggcctt cagccaaccc aaatgcccag 180
cccacggact tcgacttcct caaagtcata ggcaaaggga actacgggaa ggtcctactg 240
gccaagcgca agtctgatgg ggcgttctat gcagtgaagg tactacagaa aaagtccatc 300
ttaaagaaga aagagcagag ccacatcatg gcagagcgca gtgtgcttct gaagaacgtg 360
cggcaccctt tcctcgtggg cctgcgctac tccttcaga cacctgagaa gctctaactc 420
gtgctcgact atgtcaacgg gggagagctc ttcttcacc tgcagcggga gcgccggttc 480
ctggagcccc gggccagggt ctacgctgct gaggtggcca gcgccattgg ctacctgcac 540
tcctcaaca tcatttacag ggatctgaaa ccagagaaca ttctcttga ctgccaggga 600
cacgtggtgc tgacggattt tggcctctgc aaggaagggt tagagcctga agacaccaca 660
tccacattct gtggtacccc tgagtacttg gcacctgaag tgcttcggaa agagccttat 720
gatcgagcag tggactggtg gtgcttgggg gcagtcctct acgagatgct ccatggcctg 780
ccgcccttct acagccaaga tgtatcccag atgtatgaga acattctgca ccagccgcta 840
cagatccccg gagggccggac agtggccgcc tgtgacctcc tgcaaagcct tctccacaag 900
gaccagaggc agcggctggg ctccaaagca gactttcttg agattaagaa ccatgtattc 960
ttcagcccca taaactggga tgacctgtac cacaagaggc taactccacc cttcaaccca 1020
aatgtgacag gacctgctga cttgaagcat tttgaccag agttcaccca ggaagctgtg 1080
tccaagtcca ttggctgtac ccctgacact gtggccagca gctctggggc ctcaagtgca 1140
ttcctgggat tttcttatgc gccagaggat gatgacatct tggattgcta gaagagaagg 1200
acctgtgaaa ctactgaggc cagctggtat tagtaaggaa ttaccttcag ctgctaggaa 1260
gagcgactca aactaacaat ggcttcaacg agaagcaggt ttatTTTTTt cagcacataa 1320

aagaaaaata atgtttcgga gtccaggact ggcaggacag gtcacagat actcagaggc 1380
tgtatctctg ccctgccaac cttgacaaat ggcttccaat gttaggtttg ctacaagatg 1440
gttactggag ctctagctgc ctattttgtg tttagggaag ggaaaatgga ggaaagggga 1500
gaagagcaaa gggcgctttt aaagagcttt cccaaaagct ccccccaatg acttttgctt 1560
ccatctcact aaccacccac ccctacctgg aatggaggct gggaaatgtg gcttatttgc 1620
tgggtacgtg actatcccta ataacaaagg ggttttgacc ctaagacatt aggggagaat 1680
gttgggtagg cagccagccc tcttttacca tagggcctcc tgggtgttgg attttgatct 1740
caatgtgtaa aatgacagag atgtaacaag ctcatagggt atcaatatct cttattgttc 1800
tatgttgaaa aaaaaaaaaa aaaaaaaaaa aaaa 1834

<210> 8

<211> 427

<212> PRT

<213> h. sapiens

<400> 8

Met	Gln	Gly	Leu	Leu	Thr	Ser	Gly	Arg	Lys	Pro	Ser	Gly	Gly	Gly	Arg
1				5					10					15	
Cys	Thr	Gly	Arg	Gly	Gly	Trp	Arg	Gly	Gln	Trp	Cys	Leu	Lys	Pro	Trp
			20					25					30		
Met	Gly	Gly	Ala	Asp	Pro	Pro	Thr	Pro	Thr	Leu	Ser	Cys	Leu	Leu	Leu
		35					40					45			
Pro	Val	Pro	Pro	Glu	Leu	Pro	Asp	His	Cys	Tyr	Arg	Met	Asn	Ser	Ser
	50					55					60				
Pro	Ala	Gly	Thr	Pro	Ser	Pro	Gln	Pro	Ser	Arg	Ala	Asn	Gly	Asn	Ile
	65				70					75					80
Asn	Leu	Gly	Pro	Ser	Ala	Asn	Pro	Asn	Ala	Gln	Pro	Thr	Asp	Phe	Asp
				85					90					95	
Phe	Leu	Lys	Val	Ile	Gly	Lys	Gly	Asn	Tyr	Gly	Lys	Val	Leu	Leu	Ala
		100					105						110		
Lys	Arg	Lys	Ser	Asp	Gly	Ala	Phe	Tyr	Ala	Val	Lys	Val	Leu	Gln	Lys
		115					120					125			

Lys	Ser	Ile	Leu	Lys	Lys	Lys	Glu	Gln	Ser	His	Ile	Met	Ala	Glu	Arg		
130						135					140						
Ser	Val	Leu	Leu	Lys	Asn	Val	Arg	His	Pro	Phe	Leu	Val	Gly	Leu	Arg		
145				150						155					160		
Tyr	Ser	Phe	Gln	Thr	Pro	Glu	Lys	Leu	Tyr	Phe	Val	Leu	Asp	Tyr	Val		
				165					170					175			
Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Gln	Arg	Glu	Arg	Arg	Phe	Leu		
			180					185					190				
Glu	Pro	Arg	Ala	Arg	Phe	Tyr	Ala	Ala	Glu	Val	Ala	Ser	Ala	Ile	Gly		
		195					200					205					
Tyr	Leu	His	Ser	Leu	Asn	Ile	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn		
	210					215					220						
Ile	Leu	Leu	Asp	Cys	Gln	Gly	His	Val	Val	Leu	Thr	Asp	Phe	Gly	Leu		
225					230					235					240		
Cys	Lys	Glu	Gly	Val	Glu	Pro	Glu	Asp	Thr	Thr	Ser	Thr	Phe	Cys	Gly		
				245					250					255			
Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Arg	Lys	Glu	Pro	Tyr	Asp		
			260					265					270				
Arg	Ala	Val	Asp	Trp	Trp	Cys	Leu	Gly	Ala	Val	Leu	Tyr	Glu	Met	Leu		
		275					280					285					
His	Gly	Leu	Pro	Pro	Phe	Tyr	Ser	Gln	Asp	Val	Ser	Gln	Met	Tyr	Glu		
	290					295					300						
Asn	Ile	Leu	His	Gln	Pro	Leu	Gln	Ile	Pro	Gly	Gly	Arg	Thr	Val	Ala		
305					310					315					320		
Ala	Cys	Asp	Leu	Leu	Gln	Ser	Leu	Leu	His	Lys	Asp	Gln	Arg	Gln	Arg		
				325					330					335			
Leu	Gly	Ser	Lys	Ala	Asp	Phe	Leu	Glu	Ile	Lys	Asn	His	Val	Phe	Phe		
			340					345					350				
Ser	Pro	Ile	Asn	Trp	Asp	Asp	Leu	Tyr	His	Lys	Arg	Leu	Thr	Pro	Pro		
		355					360					365					
Phe	Asn	Pro	Asn	Val	Thr	Gly	Pro	Ala	Asp	Leu	Lys	His	Phe	Asp	Pro		
	370					375					380						
Glu	Phe	Thr	Gln	Glu	Ala	Val	Ser	Lys	Ser	Ile	Gly	Cys	Thr	Pro	Asp		
385					390					395					400		
Thr	Val	Ala	Ser	Ser	Ser	Gly	Ala	Ser	Ser	Ala	Phe	Leu	Gly	Phe	Ser		
				405					410					415			

Tyr Ala Pro Glu Asp Asp Asp Ile Leu Asp Cys
420 425

<210> 9

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 9

acacggatcc gccaccatgt atccatatga tgttccagat tatgctacgg tgaaaactga 60
ggctgctaag ggc 73

<210> 10

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 10

acacggtacc gtcgactcag aggaaagagt ccgtgggagg 40

<210> 11

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 11

gatctcggat ccactaacgg tac

23

<210> 12

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 12

cgttagtgga tccga

15

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 13

gctctggact tgggggtccca gctgggc

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 14

gttgatgttc ccattggccc tggaggg

27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 15

gctgggcatt tgggttggt gaaggcc

27

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 16

aacatccgtt tttggttgga ttgc

24

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 17

gggtagatgt tagtgtaaac

20

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 18

ataaagttct ggatacctaa ctagg

25

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 19

gaaggaatgc tctgacatct ggatgg

26

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 20

gatctgactg gtgtttttgga ctgtcc

26

<210> 21

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 21

ggatccagct gcctgatcat tgctac

26

<210> 22

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 22

gcggccgcct agcaatccaa gatgtcatc

29

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 23

ggatcccagg ggttgcttac ctcggg

26

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 24

gcggccgcct agcaatccaa gatgtcatc

29

<210> 25

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 25

ggatccaagc cctgaagaag attcctgcc

29

<210> 26

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 26

ggatccaagc cctgaagaag attcctgcc

29

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 27

gcggccgctc acaaaaataa gtcttc

26

<210> 28

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 28

ggatcctgga cagtccaaaa caccag

26

<210> 29

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR PRIMER

<400> 29

gcggccgctc acaaaaataa gtcttc

26

<210> 30

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 30

Gly Arg Pro Arg Thr Ser Ser Phe Ala Glu Gly
1 5 10

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 31

Arg Pro Arg Thr Ser Ser
1 5

<210> 32

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 32

Arg Pro Arg Thr Ser Ala Phe
1 5

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 33

Pro Arg Thr Ser Ser Phe
1 5

<210> 34

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 34

Arg Pro Arg Thr Ser Ser
1 5

<210> 35

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 35

Arg Pro Arg Thr Ser Thr Phe
1 5

<210> 36

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 36

Arg Pro Arg Ala Ala Thr Phe
1 5

<210> 37

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 37

Lys Pro Arg Thr Ser Ser Phe
1 5

<210> 38

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 38

Arg Pro Lys Thr Ser Ser Phe
1 5

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 39

Arg Pro Arg Thr Ser Ser Phe
1 5

<210> 40

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 40

Arg Pro Arg Thr Ser Ser Leu
1 5

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 41

Arg Pro Arg Thr Ser Ser Val
1 5

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 42

Arg Pro Arg Thr Ser Ser Ala
1 5

<210> 43

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 43

Arg Pro Arg Thr Ser Ser Lys
1 5

<210> 44

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PEPTIDE

<400> 44

Arg Pro Arg Thr Ser Ser Glu
1 5

By
Conte sub C/H
cont

C